

[illegible]

FIGURE 1A

334	343	352	361	370	379
CAT GAG CCG	CCA GAG CCC	GAG GAG ATC	ACT GGC CCT	GTG GAT GAG	GAG ACC
H E P	P E P	E E I	T G P	V D E	E T
388	397	406	415	424	433
TTC CTG AAA	GCT GGG GAG	GGG AAA ATG	AAG GTC ATT	GAG AAG TTC	CTG GCT
F L K	A A V	E G K	M K V	I E K	F L A
442	451	460	469	478	487
GAC GGG TCA	GCC GAC ACG	TGC GAC CAG	TTC CGT CGG	ACA GCA CTG	CAC CGA
D G G	S A D	T C D	Q F R	T A L	H R
496	505	514	523	532	541
GCT TCC CTG	GAA GGC CAC	ATG GAA ATC	CTG GAG AAG CTT	CTA GAT AAT	GGG GCC
A S L	E G H	E I L	E K L	L D N	G A
550	559	568	577	586	595
ACT GTG GAC	TTC CAG GAT	CGG CTG GAC	TGC ACA GCC	ATG CAT TGG	GCC TGC
T V D	F Q D	R L D	C T A	M H W	A C R
604	613	622	631	640	649
GGG GGC CAC	TTA GAG GTG	AAA CTT CTG	CAA AGC CAT	GGA GCA GAC	ACC AAT
G G H	L E V	V K L	L Q S	H G A	D T N

FIGURE 1B

658	667	676	685	694	703
GTG AGG	AAG CTG	AGC ACC	CTG CAC	GTG GCA	GTG GCA
V R D	K L L	S T P	L H V	A V R	T G Q
712	721	730	739	748	757
GTG GAG	ATG GAG	CTA TCC	CTG GGC	CTG GAA	ATC GGC
V E I	V E H	F L S	L G L	E I N	A R D
766	775	784	793	802	811
AGG GAA	GGG GAT	ACT GCC	CTG GCT	GTG AGG	CTC AAC
R E G	D T A	L H D	A V R	L N R	Y K I
820	829	838	847	856	865
ATC AAA	CTG CTC	CTG CAT	GGG GCT	GAC ATG	ATG ACC
I K L	L L L	H G A	D M M	T K N	L A G
874	883	892	901	910	919
AAG ACC	CCG ACG	GAC CTG	GTG CAG	TGG CAG	GCT GAT
K T P	T D L	V Q L	W Q A	D T R	H A L
928	937	946	955	964	973
GAG CAT	CCT GAG	CCG GCT	GCT GAG	CTG GGG	CTG CCT
E H P	E P G	A E H	N G L	E G P	N D S

FIGURE 1C

982	991	1000	1009	1018	1027
GGG CGA GAG ACC	CCT CAG CCT	GTG CCA GCC	CAG TGA ATG	CGT GCC CCA	GCC CAG
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G R E T	P Q P	V P A	Q		
---	---	---	---	---	---
1036	1045	1054	1063	1072	1081
CCA GCT ACC	CAG CCC CTC	TCT GTG TGC	AGC CGG AGG	GTC CTA AGA	ATG GCT CCC
---	---	---	---	---	---
1090	1099	1108	1117	1126	1135
GGA GCT AAC	TGA GGG CCC	AGC CTT TTT	TCT GCA TGA	TCC AGG AGC	ACA TAC CAC
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1144	1153				
AAA CTA CCA	CAA TAA AAA	AGC TG	3'		
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FIGURE 1D

1	S	M	E	D	S	E	A	V	Q	R	A	T	A	L	I	E	Q	R	L	A	5578191CD1
1	-	M	E	G	P	E	A	V	Q	R	A	T	E	L	I	E	Q	R	L	A	g9501360
1	-	M	E	G	P	E	A	V	Q	R	A	T	E	L	I	E	Q	R	L	A	g5420272
21	Q	E	E	N	E	K	L	R	G	D	T	R	Q	K	L	P	M	D	L	5578191CD1	
20	Q	E	E	E	T	E	K	L	R	S	A	P	G	K	L	S	M	D	M	g9501360	
20	Q	E	E	E	T	E	K	L	R	S	A	P	G	K	L	S	M	D	M	g5420272	
41	L	V	L	E	D	E	K	H	H	G	A	Q	S	A	A	L	Q	K	V	K	5578191CD1
40	L	V	L	E	E	E	K	R	L	G	V	Q	S	P	A	L	Q	K	V	K	g9501360
40	L	V	L	E	E	E	K	R	L	G	V	Q	S	P	A	L	Q	K	V	K	g5420272
61	G	Q	E	R	V	R	K	T	S	L	D	L	R	R	E	I	I	D	V	G	5578191CD1
60	G	Q	E	R	V	R	K	T	S	L	D	L	R	R	E	I	I	D	V	G	g9501360
60	G	Q	E	R	V	R	K	T	S	L	D	L	R	R	E	I	I	D	V	G	g5420272
81	G	I	Q	N	L	I	E	L	R	K	K	R	K	Q	K	K	R	D	A	L	5578191CD1
80	G	I	Q	N	L	I	E	L	R	K	K	R	K	Q	K	K	R	D	A	L	g9501360
80	G	I	Q	N	L	I	E	L	R	K	K	R	K	Q	K	K	R	D	A	L	g5420272

FIGURE 2A

101	A A S H E P P P E E I T G P V D E E	5578191CD1
100	A A Q E P P P E E I T G P V N E E	g9501360
100	A A A Q E P P P E E I T G P V N E E	g5420272
121	T F L K A A V E G K M K V I E K F L A D	5578191CD1
120	T F L K A A V E G K M K V I D K Y L A D	g9501360
120	T F L K A A V E G K M K V I D K Y L A D	g5420272
141	G G S A D T C D Q F R R T A L H R A S L	5578191CD1
140	G G S A D T C D E F R R T A L H R A S L	g9501360
140	G G S A D T C D E F R R T A L H R A S L	g5420272
161	E G H M E I L E K L L D N G A T V D F Q	5578191CD1
160	E G H M E I L E K L L E N G A T V D F Q	g9501360
160	E G H M E I L E K L L E N G A T V D F Q	g5420272
181	D R L D C T A M H W A C R G G H L E V V	5578191CD1
180	D R L D C T A M H W A C R G G H L E V V	g9501360
180	D R L D C T A M H W A C R G G H L E V V	g5420272

FIGURE 2B

201	K	L	L	Q	S	H	G	A	D	T	N	V	R	D	K	L	L	S	T	P	5578191CD1
200	R	L	L	Q	S	R	G	A	D	T	N	V	R	D	K	L	L	S	T	P	g9501360
200	R	L	L	Q	S	R	G	A	D	T	N	V	R	D	K	L	L	S	T	P	g5420272
221	L	H	V	A	V	R	T	G	Q	V	E	I	V	E	H	F	L	S	L	G	5578191CD1
220	L	H	V	A	V	R	T	G	H	V	E	I	V	E	H	F	L	S	L	G	g9501360
220	L	H	V	A	V	R	T	G	H	V	E	I	V	E	H	F	L	S	L	G	g5420272
241	L	E	I	N	A	R	D	R	E	G	D	T	A	L	H	D	A	V	R	L	5578191CD1
240	L	D	I	N	A	K	D	R	E	G	D	S	A	L	H	D	A	V	R	L	g9501360
240	L	D	I	N	A	K	D	R	E	G	D	S	A	L	H	D	A	V	R	L	g5420272
261	N	R	Y	K	I	I	K	L	L	L	L	H	G	A	D	M	M	T	K	N	5578191CD1
260	N	R	Y	K	I	I	K	L	L	L	L	H	G	A	D	M	M	A	K	N	g9501360
260	N	R	Y	K	I	I	K	L	L	L	L	H	G	A	D	M	M	A	K	N	g5420272
281	L	A	G	K	T	P	T	D	L	V	Q	L	W	Q	A	D	T	R	H	A	5578191CD1
280	L	A	G	K	T	P	T	D	L	V	Q	L	W	Q	A	D	T	R	H	A	g9501360
280	L	A	G	K	T	P	T	D	L	V	Q	L	W	Q	A	D	T	R	H	A	g5420272

FIGURE 2C

301	L	E	H	P	E	P	G	A	E	H	N	G	L	E	G	P	N	D	S	G	5578191CD1
300	L	E	H	P	E	P	E	S	E	Q	N	G	L	E	R	P	-	G	S	G	g9501360
300	L	E	H	P	E	P	E	S	E	Q	N	G	L	E	R	P	-	G	S	G	g5420272
321	R	E	T	P	Q	P	V	P	A	Q	5578191CD1										
319	R	E	T	P	Q	P	I	P	A	Q	g9501360										
319	R	E	T	P	Q	P	I	P	A	Q	g5420272										

FIGURE 2D

Tissue Distribution

Tissue Category	Clone Count	Found in	Abs Abund	Pct Abund
Cardiovascular System	266190	4/68	4	0.0015
Connective Tissue	144645	0/47	0	0.0000
Digestive System	501101	1/148	1	0.0002
Embryonic Structures	106713	0/21	0	0.0000
Endocrine System	225386	2/53	2	0.0009
Exocrine Glands	254635	0/64	0	0.0000
Genitalia, Female	427284	0/106	0	0.0000
Genitalia, Male	448207	3/114	7	0.0016
Germ Cells	38282	0/5	0	0.0000
Hemic and Immune System	680277	0/159	0	0.0000
Liver	109378	0/35	0	0.0000
Musculoskeletal System	159280	10/47	24	0.0151
Nervous System	955753	4/198	5	0.0005
Pancreas	110207	0/24	0	0.0000
Respiratory System	390086	1/93	2	0.0005
Sense Organs	19256	0/8	0	0.0000
Skin	72292	0/15	0	0.0000
Stomatognathic System	12923	0/10	0	0.0000
Unclassified/Mixed	120926	1/13	1	0.0008
Urinary Tract	279062	3/64	5	0.0018
Totals	5321883	29/1292	51	0.0000

FIGURE 3A

Found in:

Library ID	Clone Count	Library Description	Abs Abund	Pct Abund
MUSCNOT10	3302	muscle, gluteal, mw/clear cell SAR, 43F	11	0.3331
MUSLTDT01	804	muscle, thigh, mw/lipoSAR, 58M	1	0.1244
MUSCNOT02	2541	muscle, psoas, 12M	3	0.1181
MUSLNOT01	3306	muscle, tibial, aw/thrombosis, 41F	2	0.0605
MUSLTDR02	4002	muscle, thigh, mw/lipoSAR, 58M, RP	2	0.0500
MUSCNO01	2716	muscle, skeletal, mw/malignant hyperthermia	1	0.0368
MUSCDIN06	3043	muscle, thigh, ALS, 74F, NORM	1	0.0329
MUSCDMT01	3137	muscle, calf, mw/gangrene, aw/atherosclerosis	1	0.0319
MUSCDIT06	3192	muscle, skeletal, aw/Krabbe, 11mf	1	0.0313
MUSCNOT07	6491	muscle, forearm, mw/intramuscular hemangioma	1	0.0154

FIGURE 3B

FOOTD' 66585260

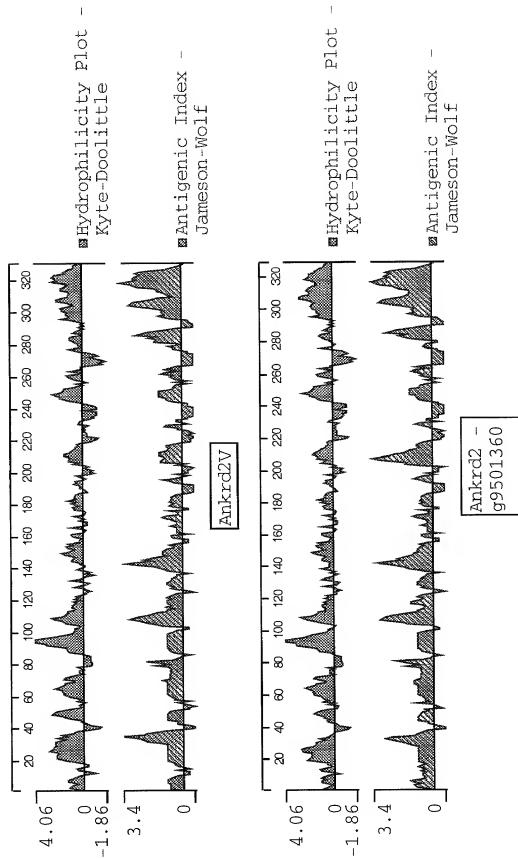


FIGURE 4A

100110-6685260

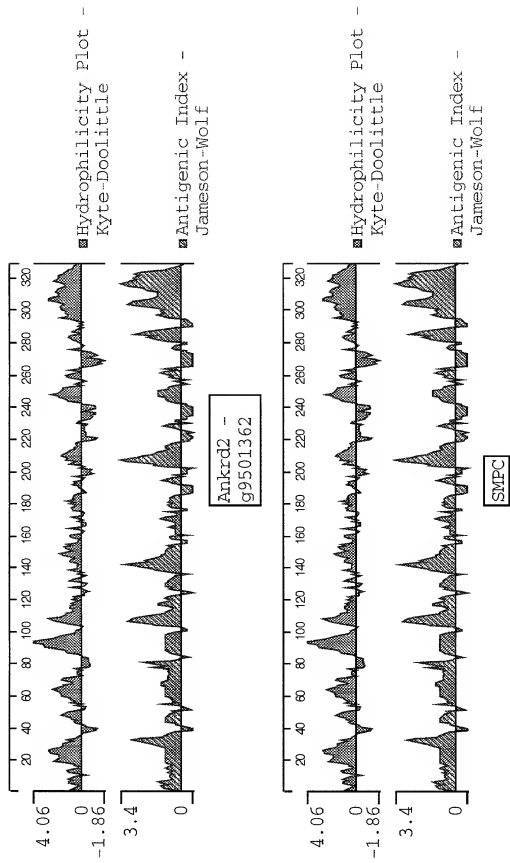


FIGURE 4B